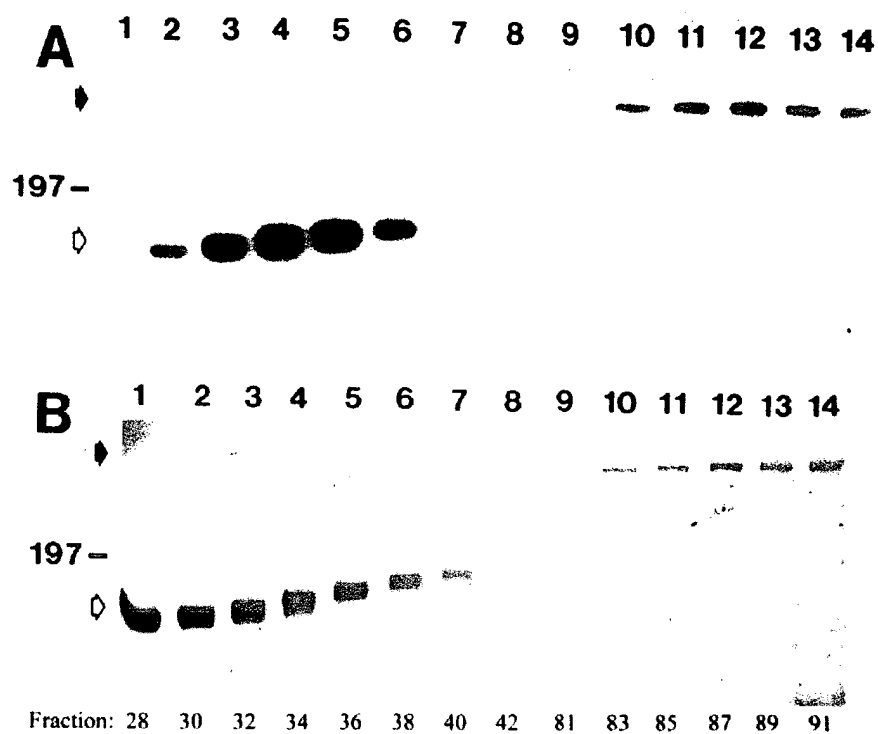
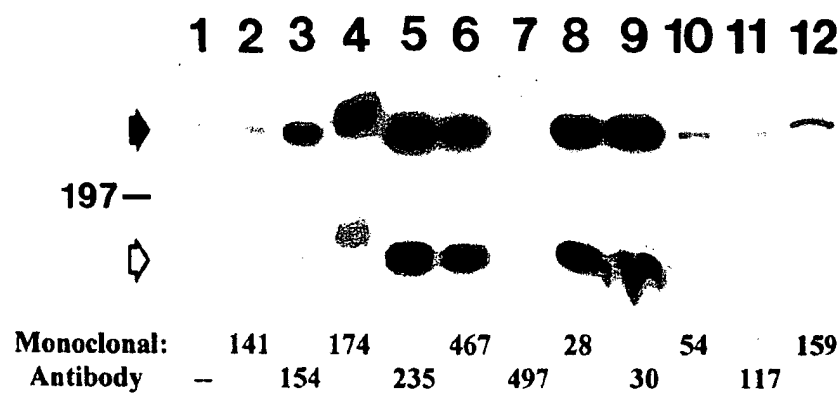


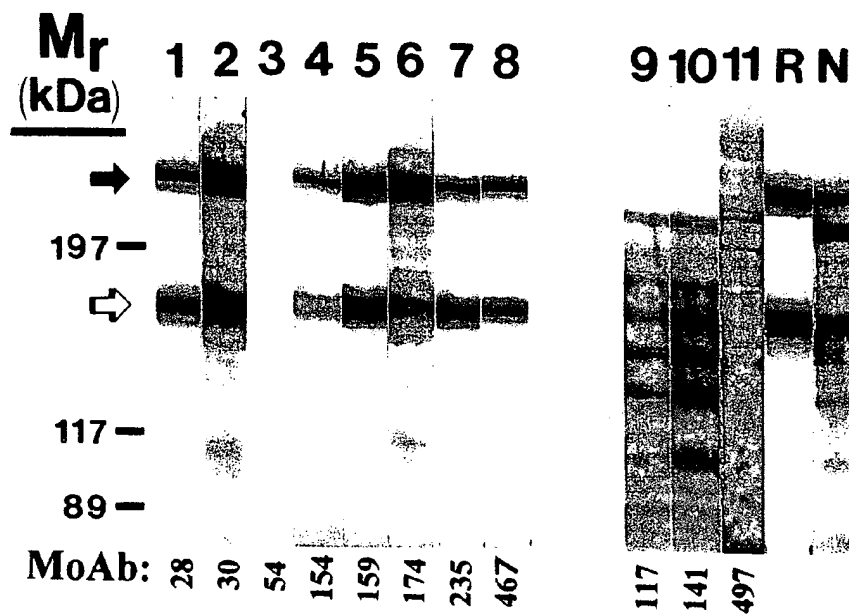
# Figure 1



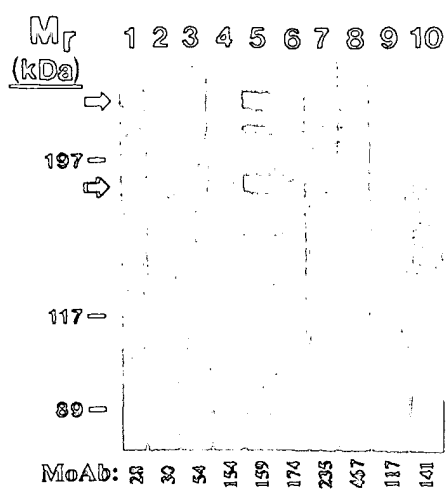
# Figure 2



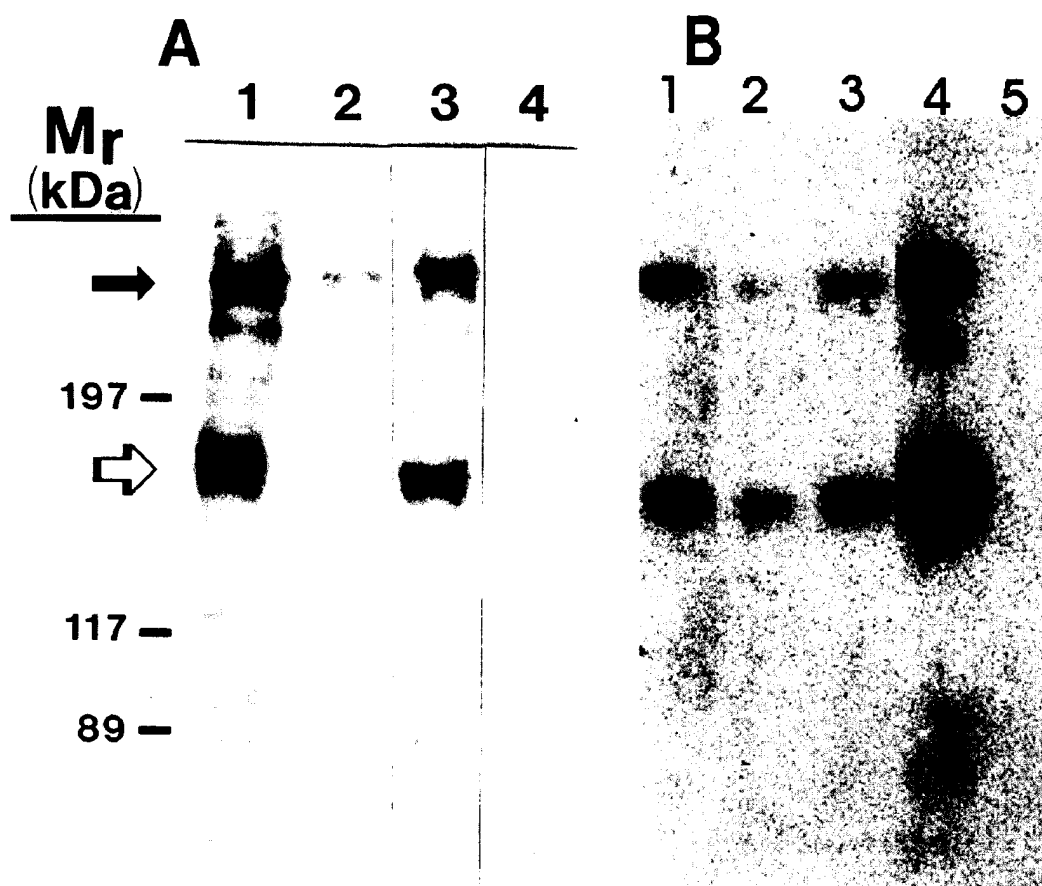
# Figure 3



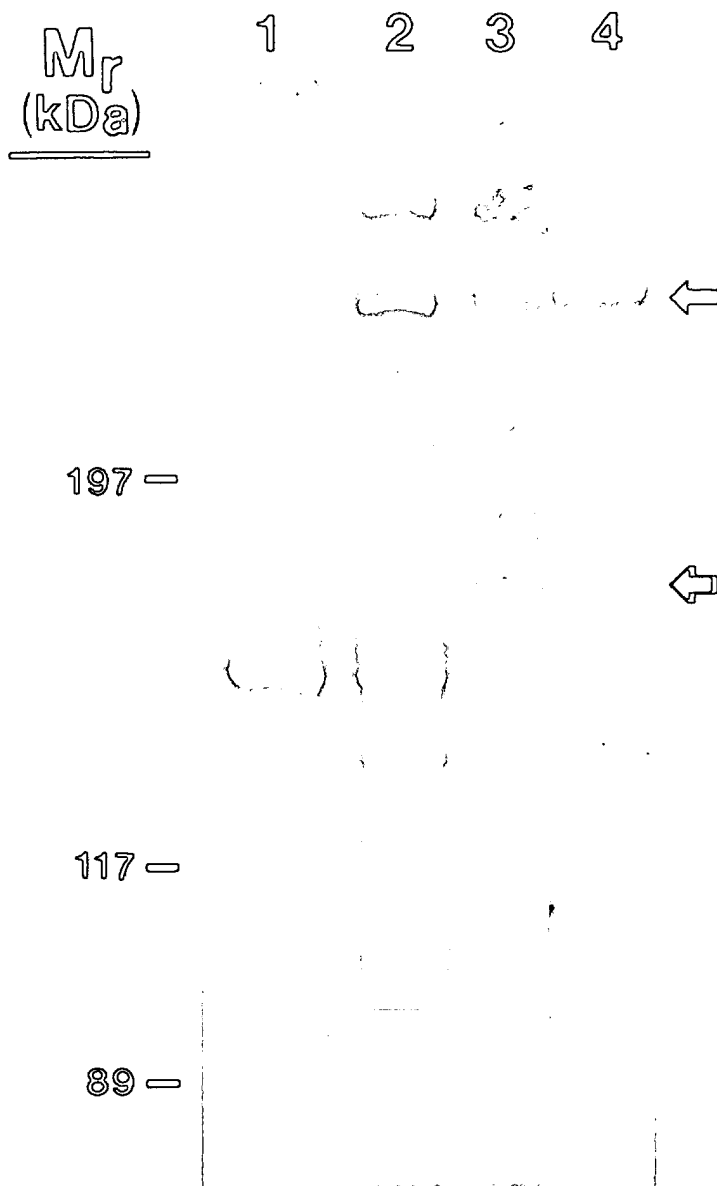
# Figure 4



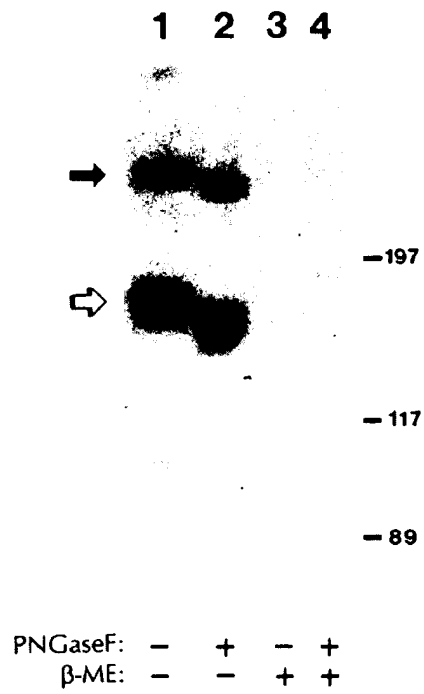
# Figure 5



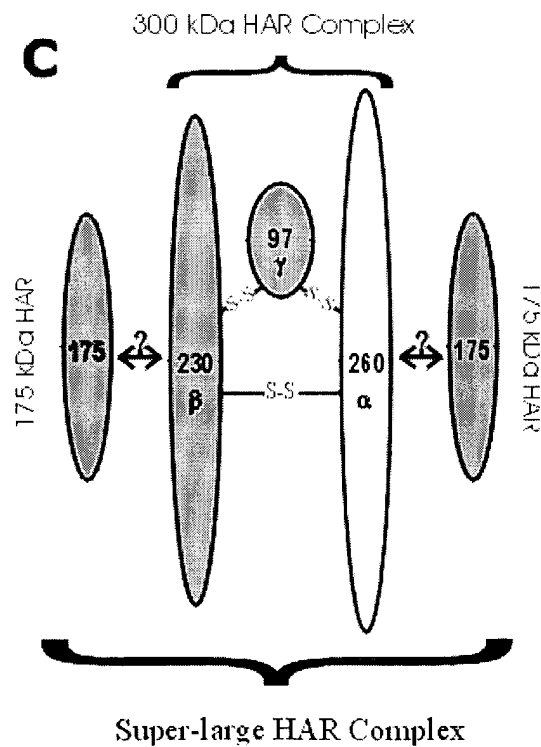
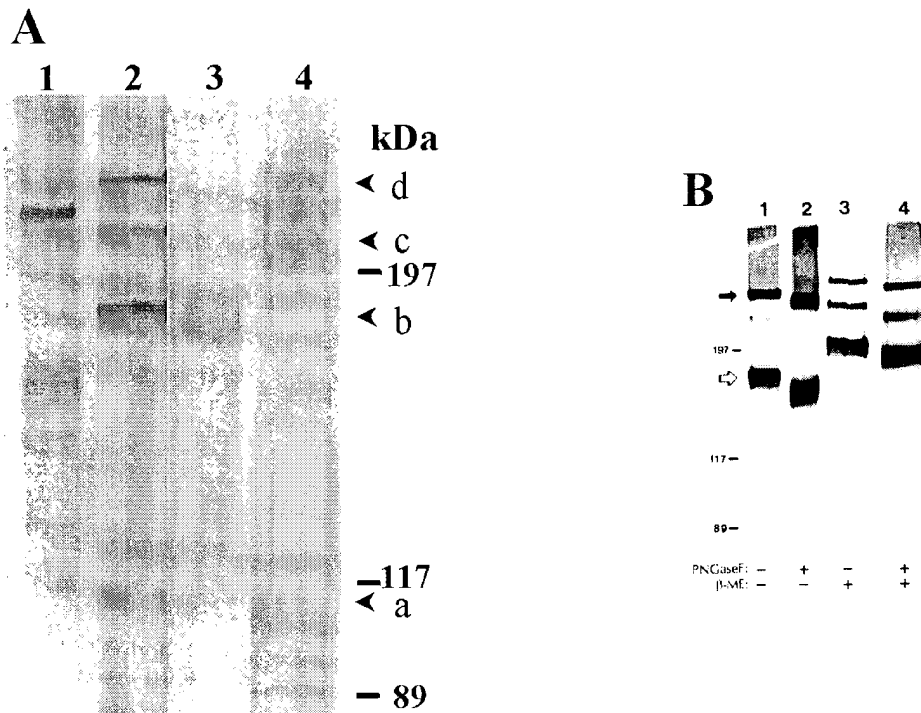
# Figure 6



# Figure 7



# Figure 8





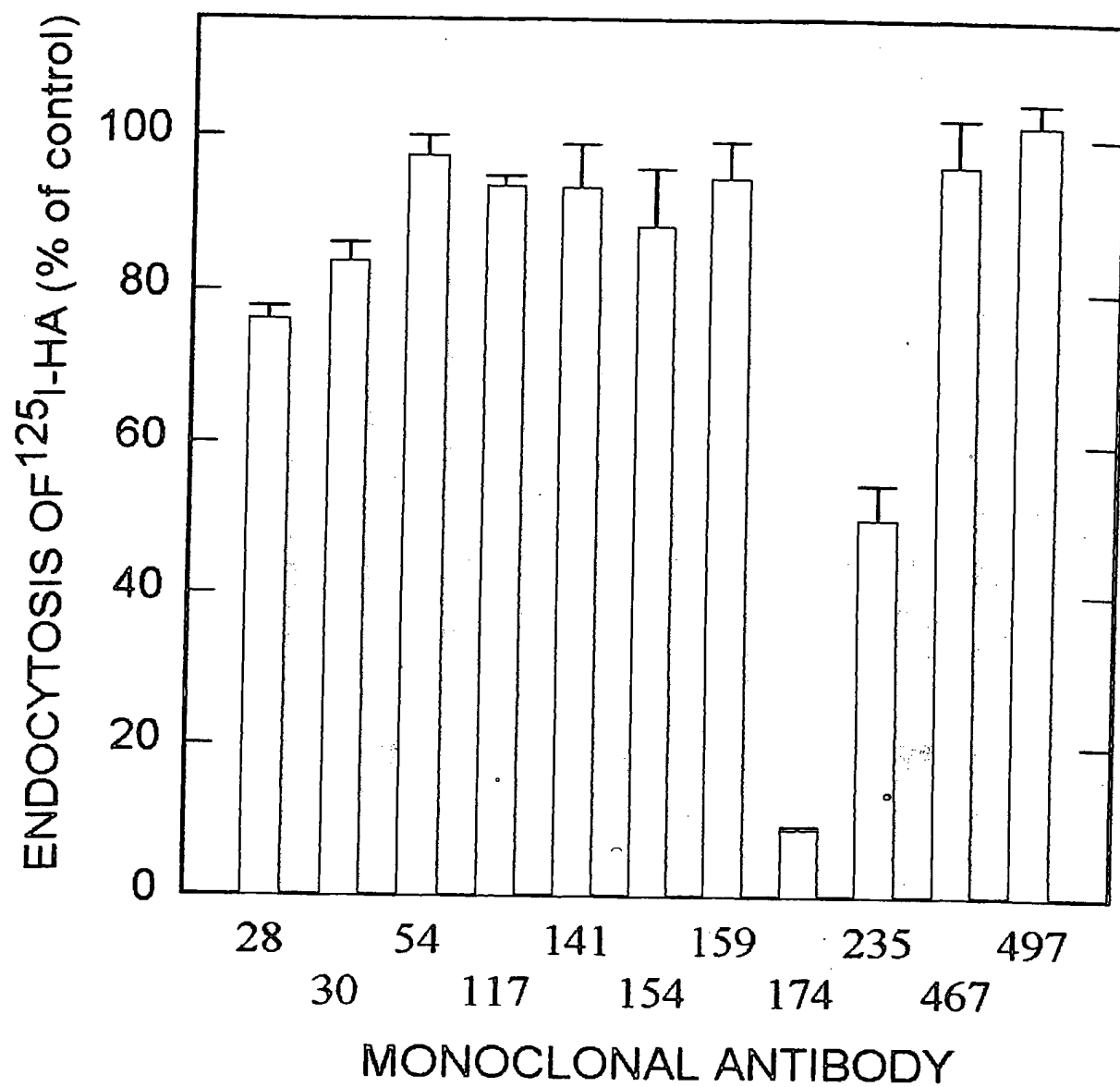


Figure 9

# Figure 10

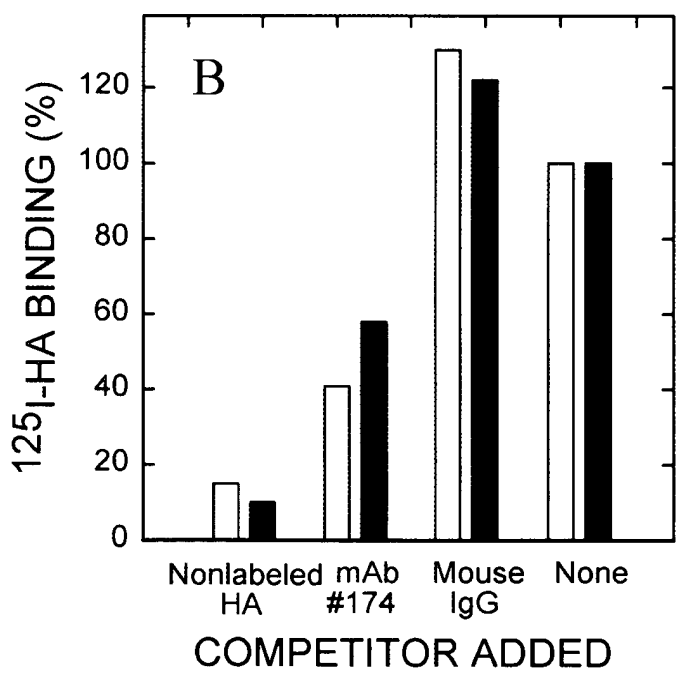
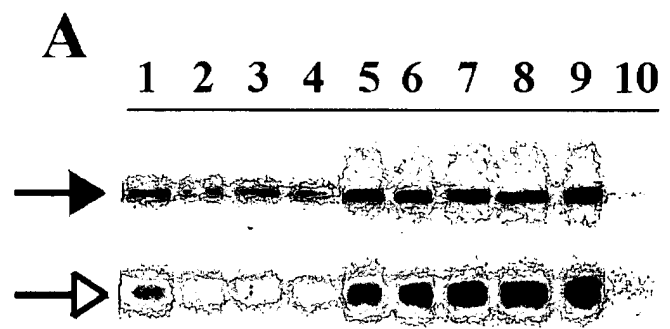


Figure 11

Antibody Inhibition of HA  
Endocytosis by HARE in LECs

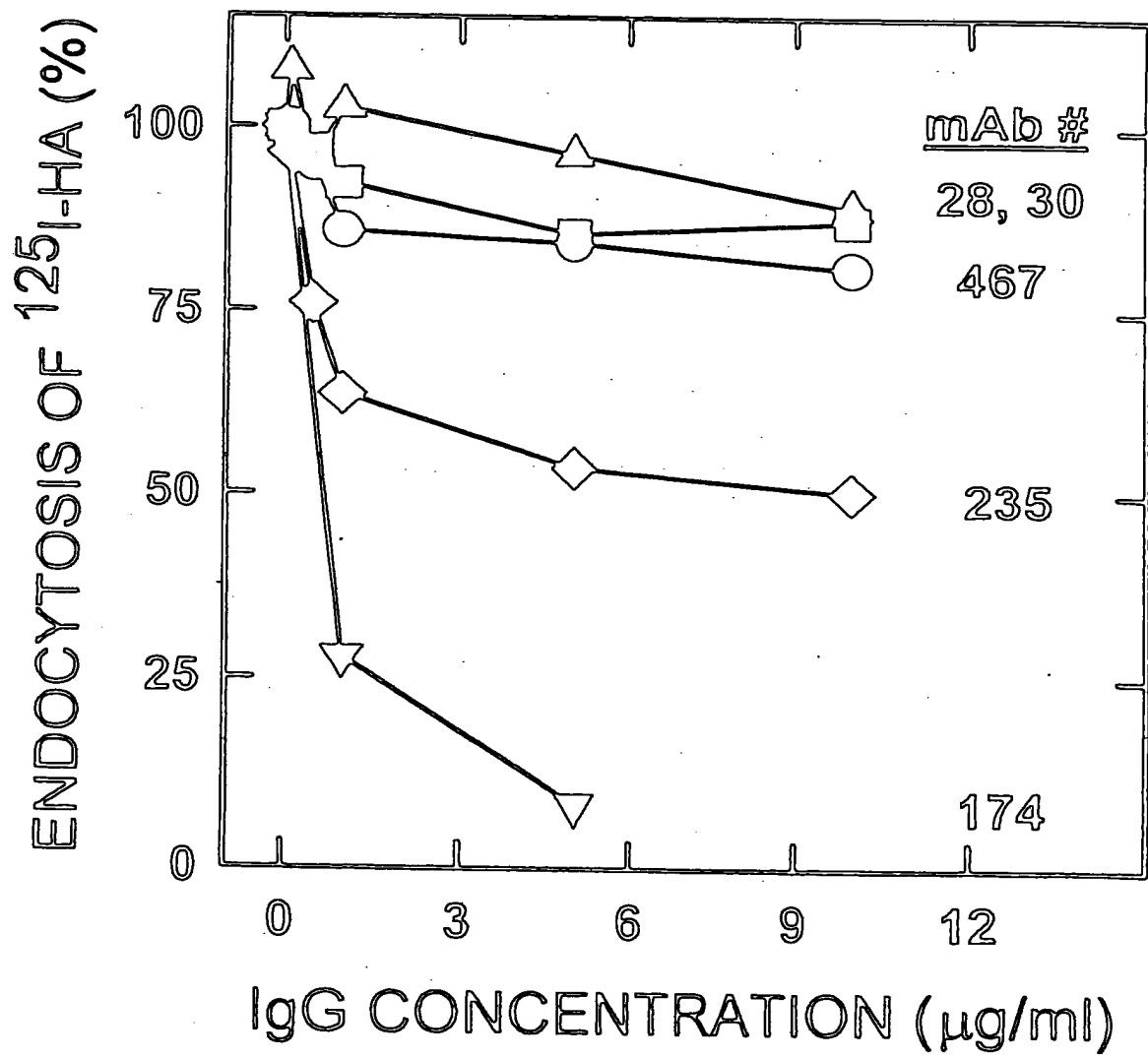
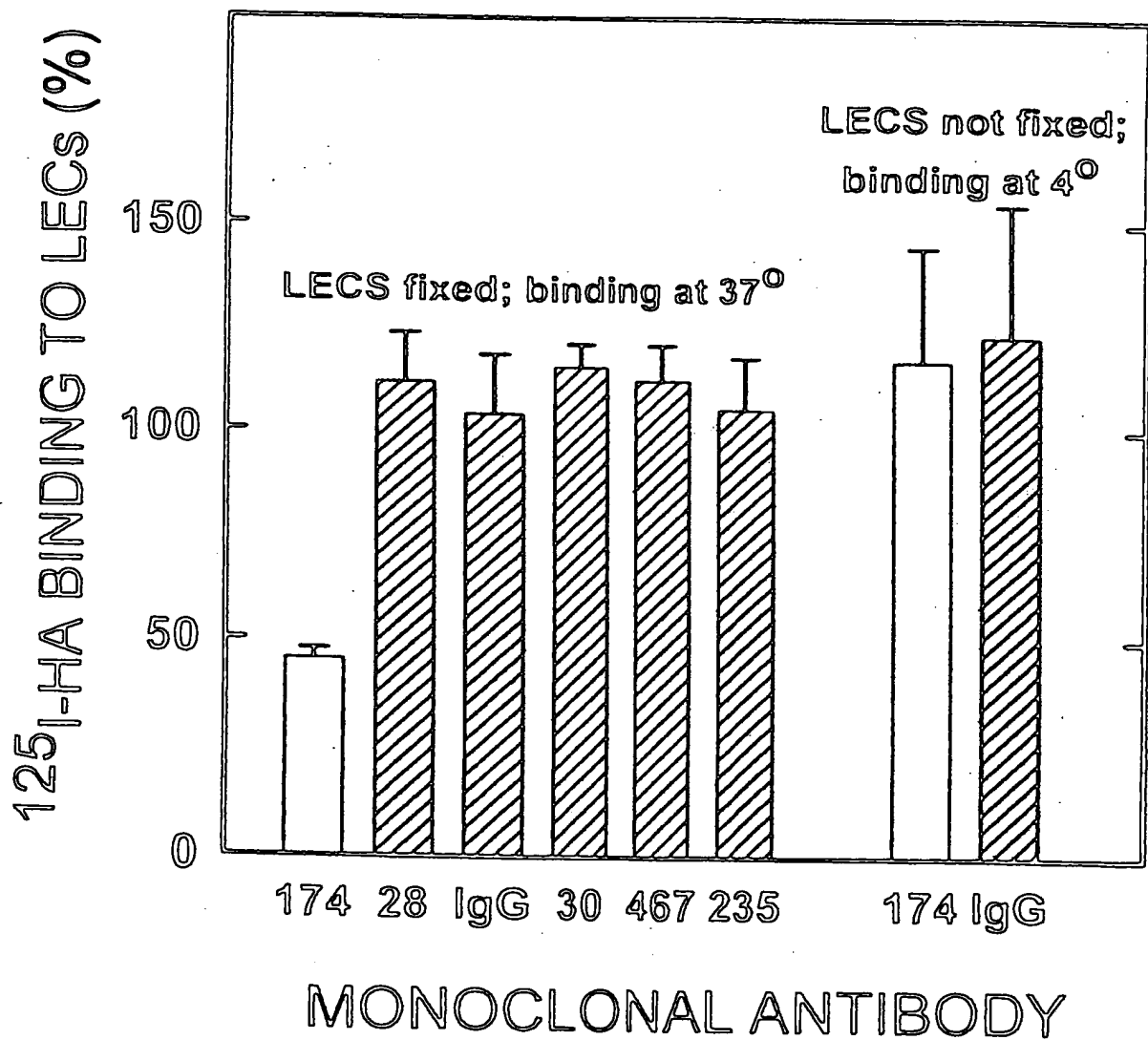


Figure 12

Antibody Inhibition of HA Binding to HARE  
on LECs is Temperature Dependent



# Figure 13

Figure 13

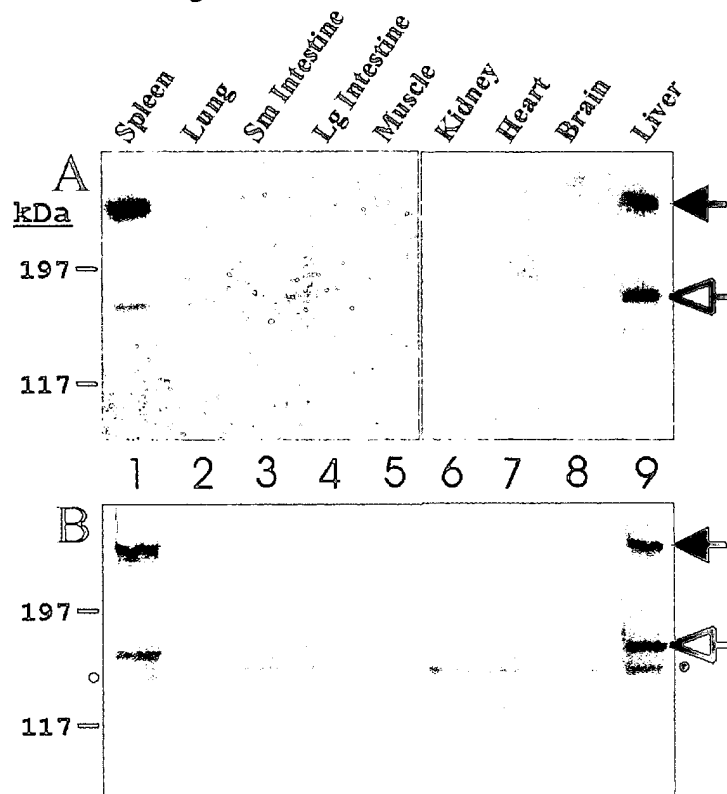
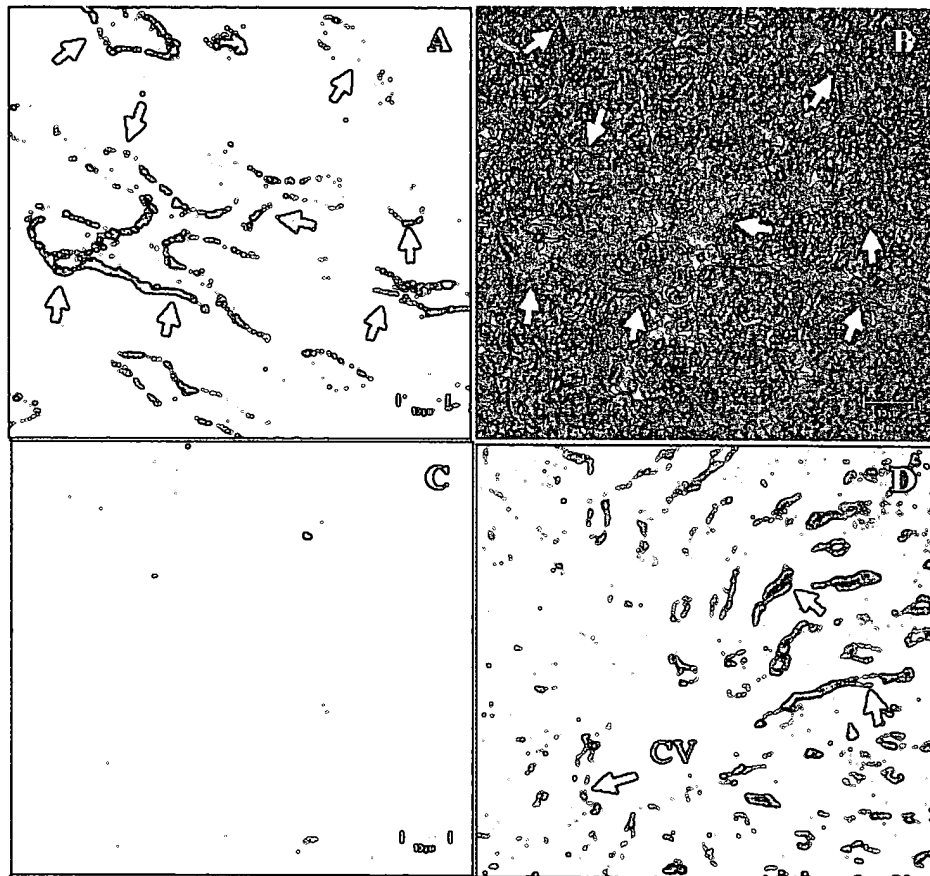


Figure 14



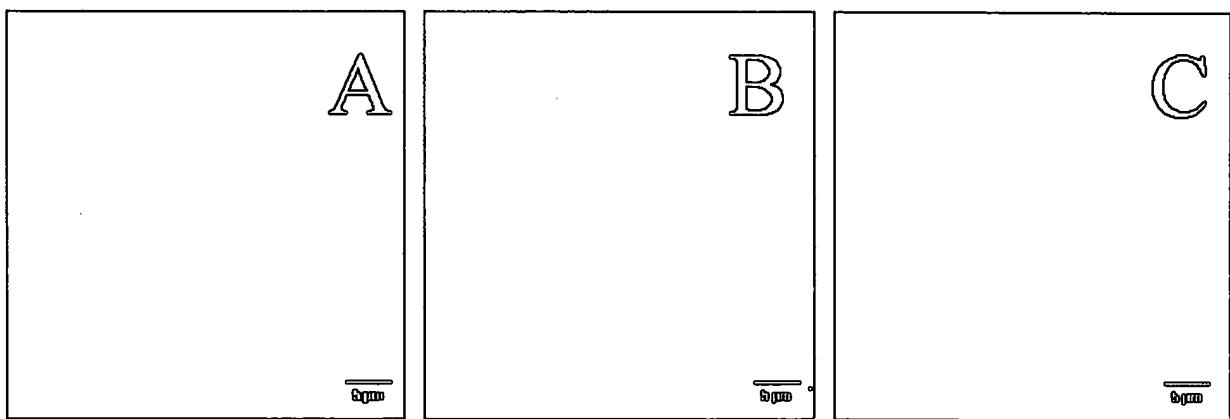
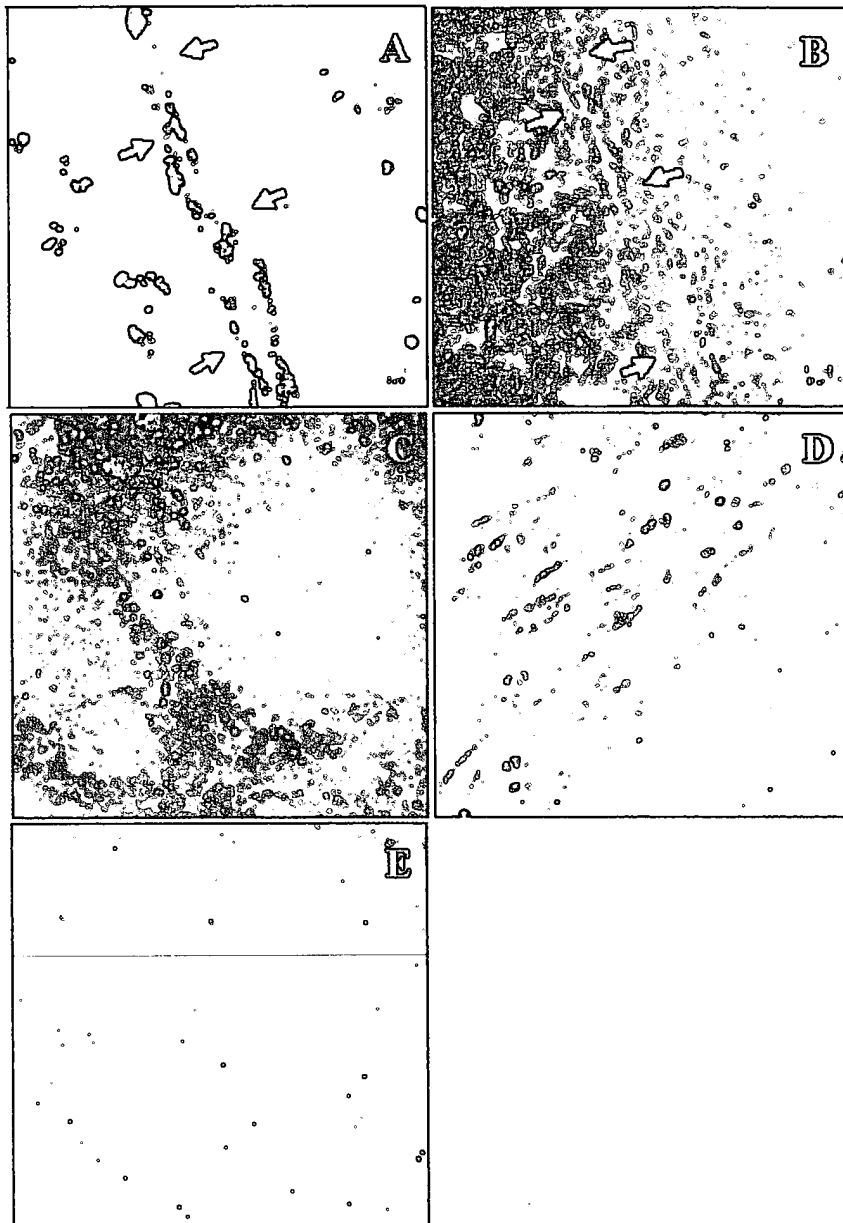


Figure 15

Figure 16





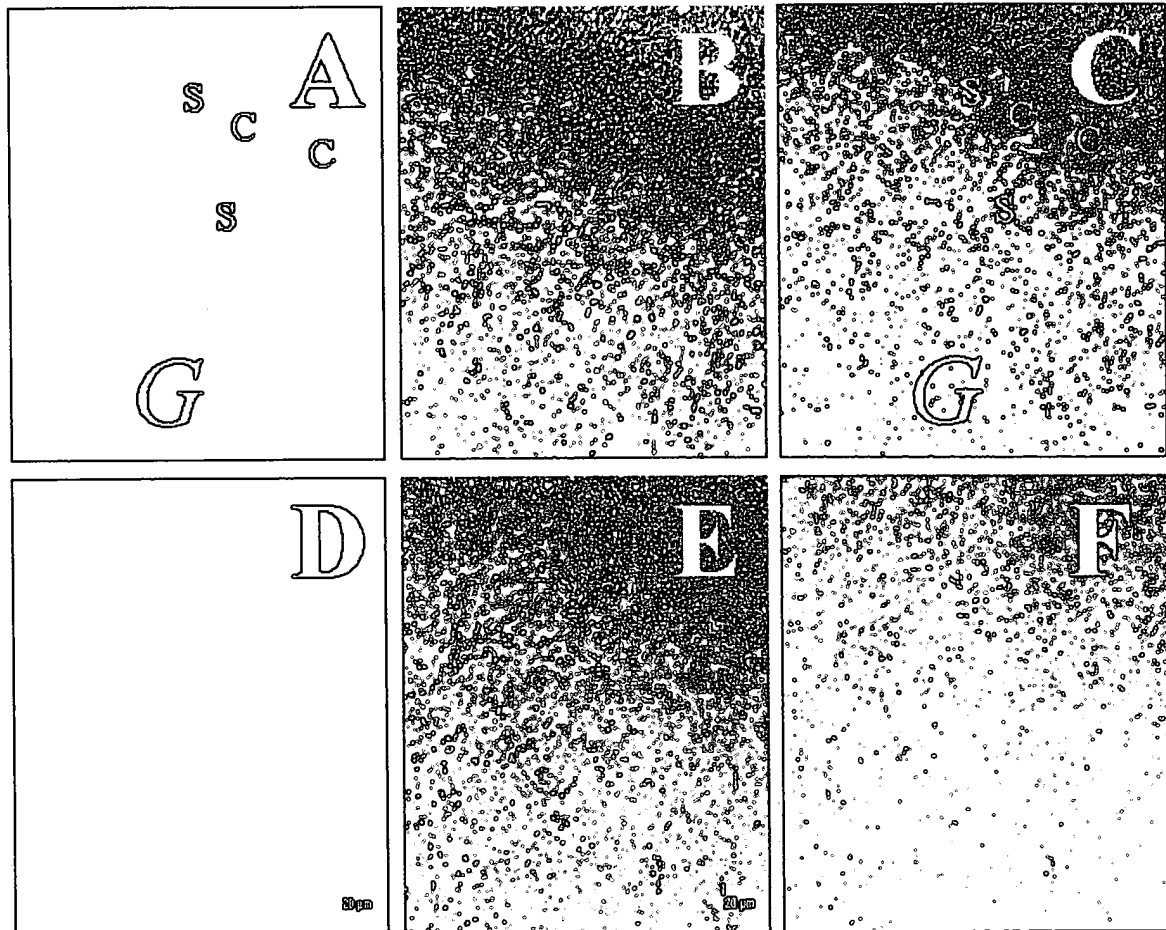
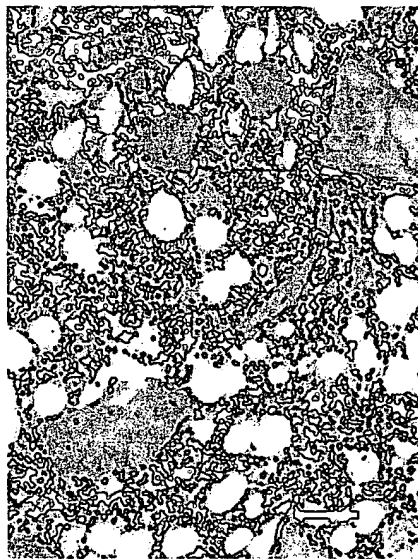


Figure 17

## Figure 18

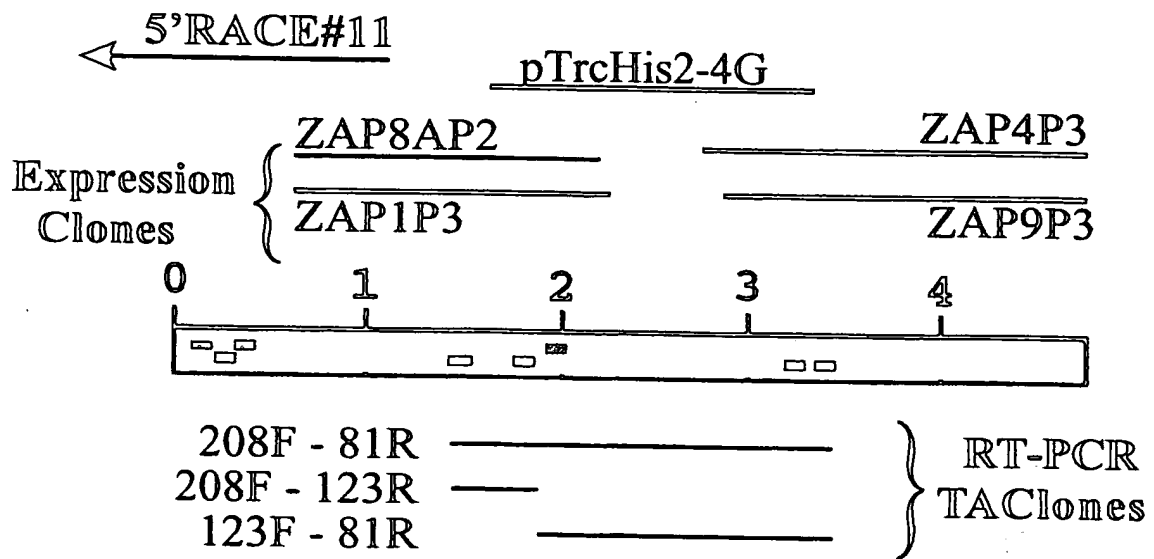
### Immunolocalization of HARE in Bone Marrow

Control



Bars = 50  $\mu$ m

Figure 19



**Figure 20**

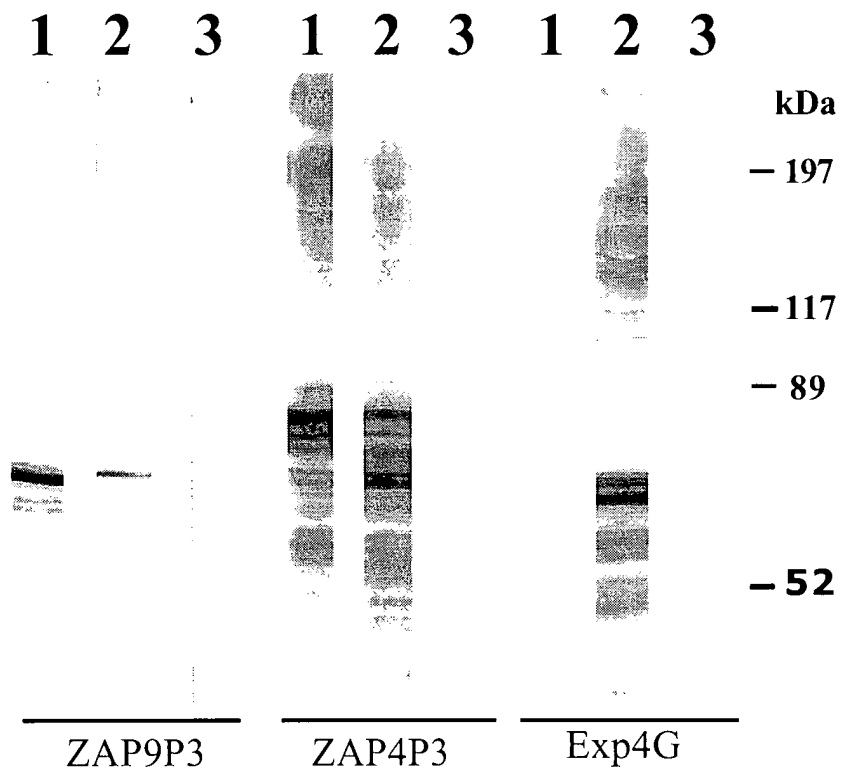
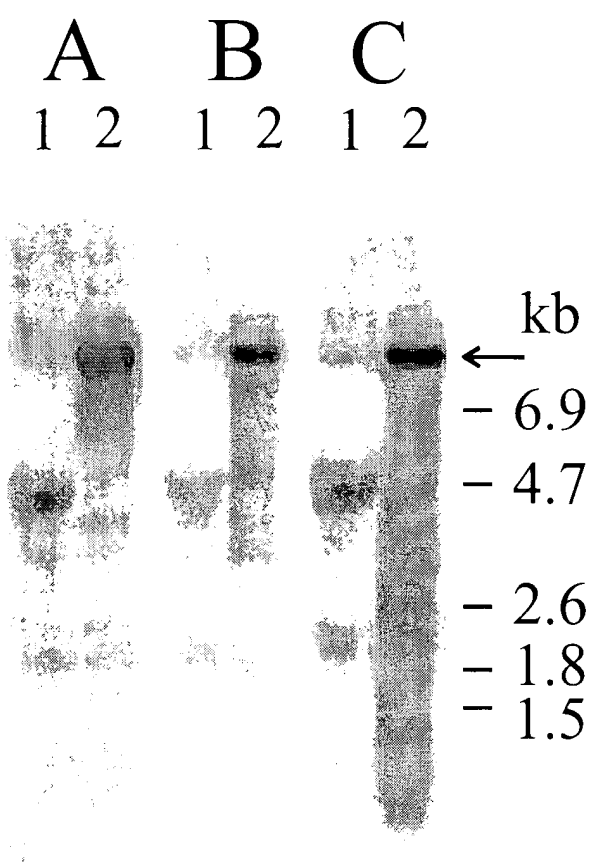
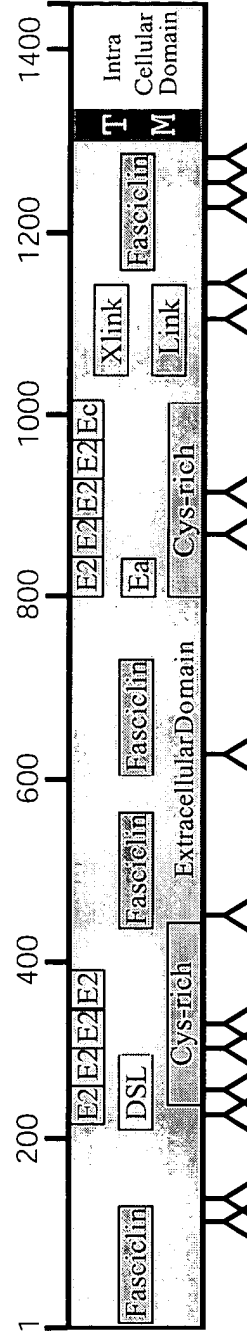




Figure 22



**Figure 23**







**Figure 25**

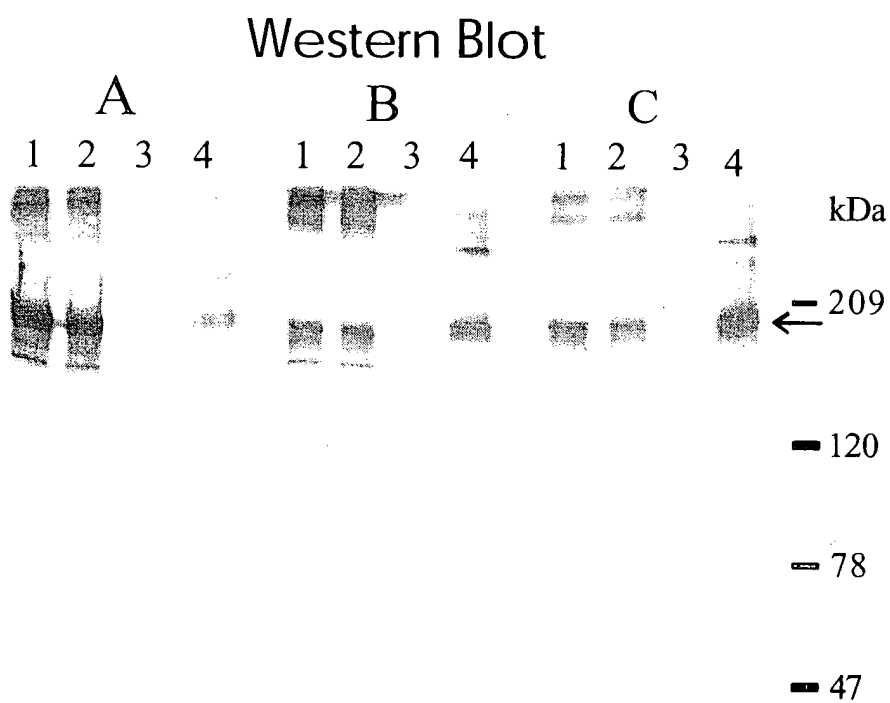
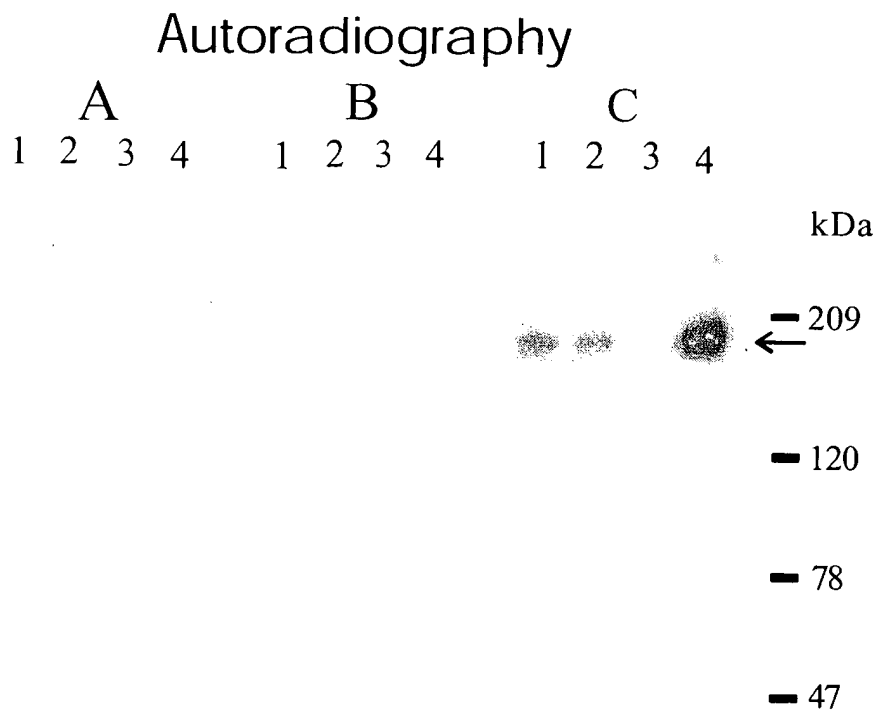


Figure 26

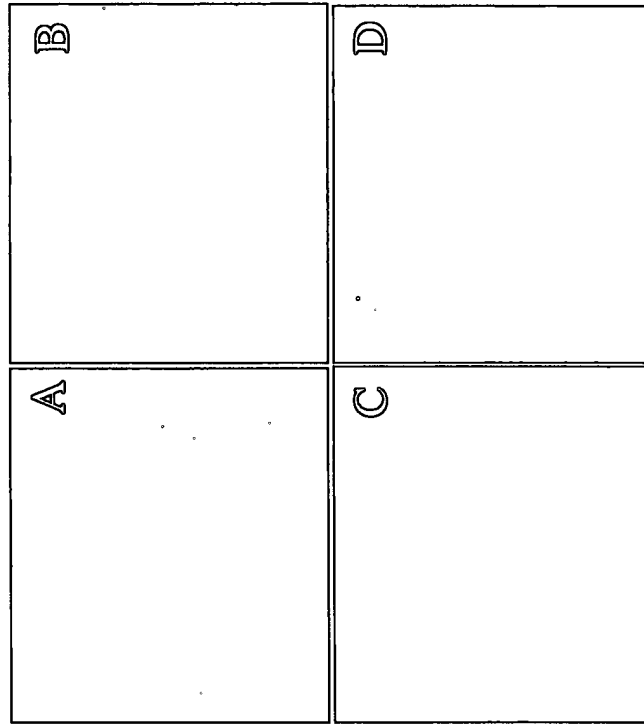


Figure 27A

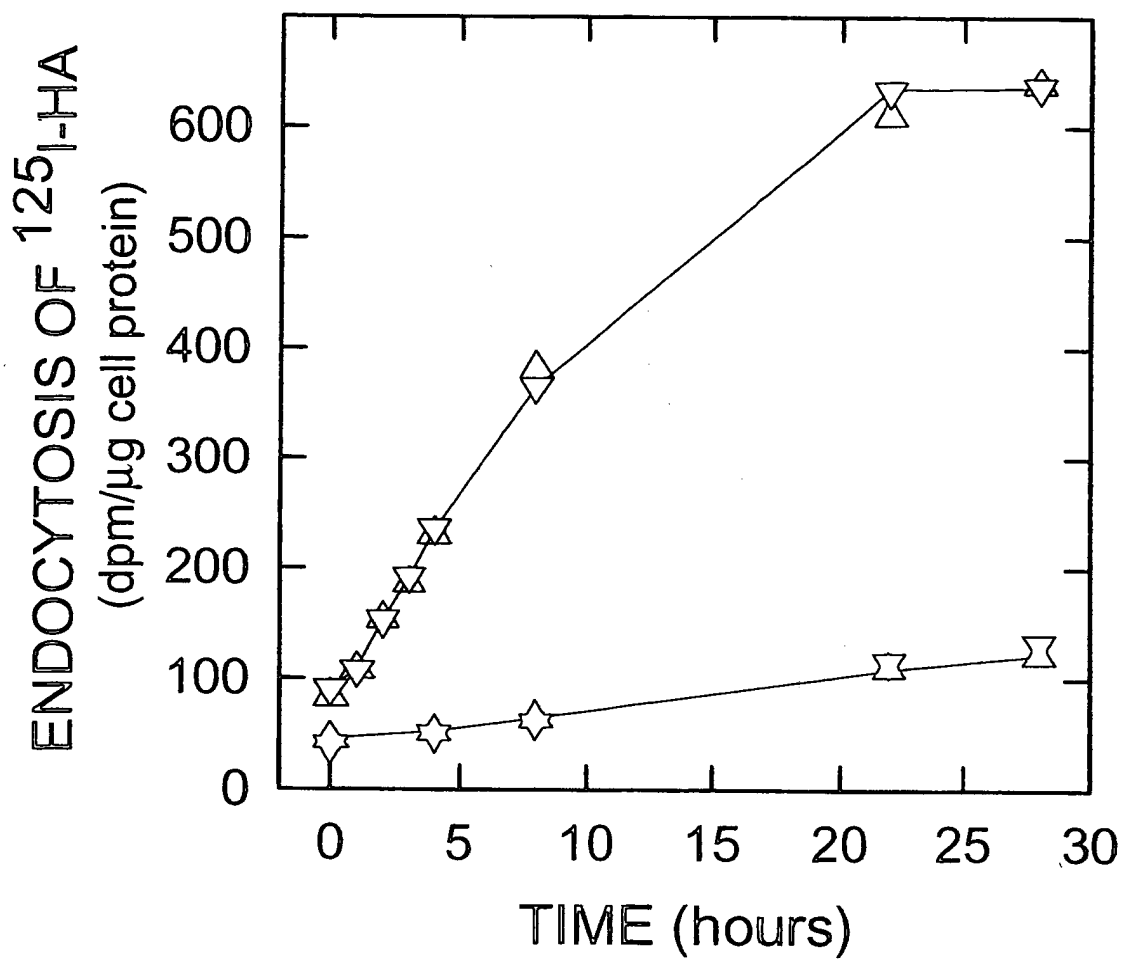


Figure 27B

**Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE**

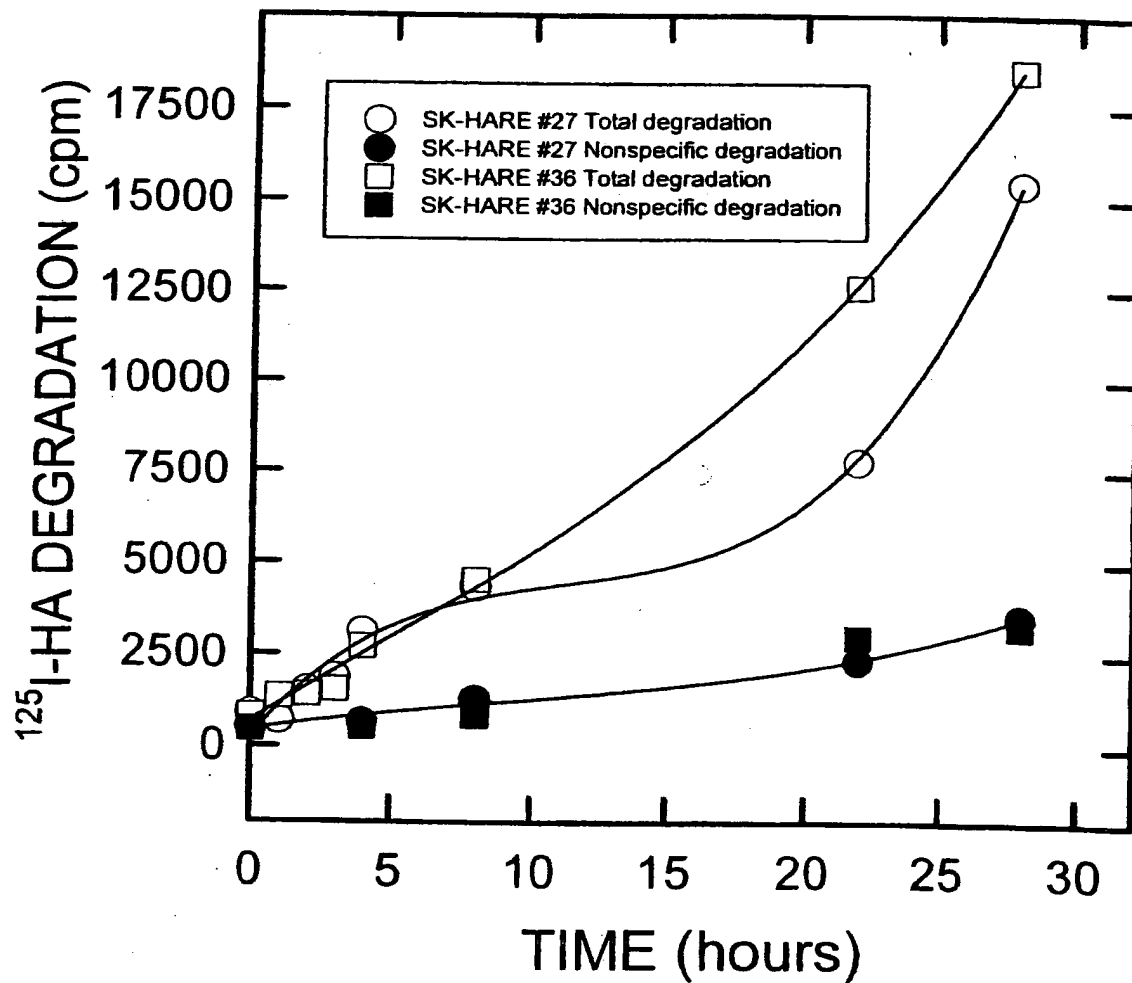


Figure 27C

**Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells**

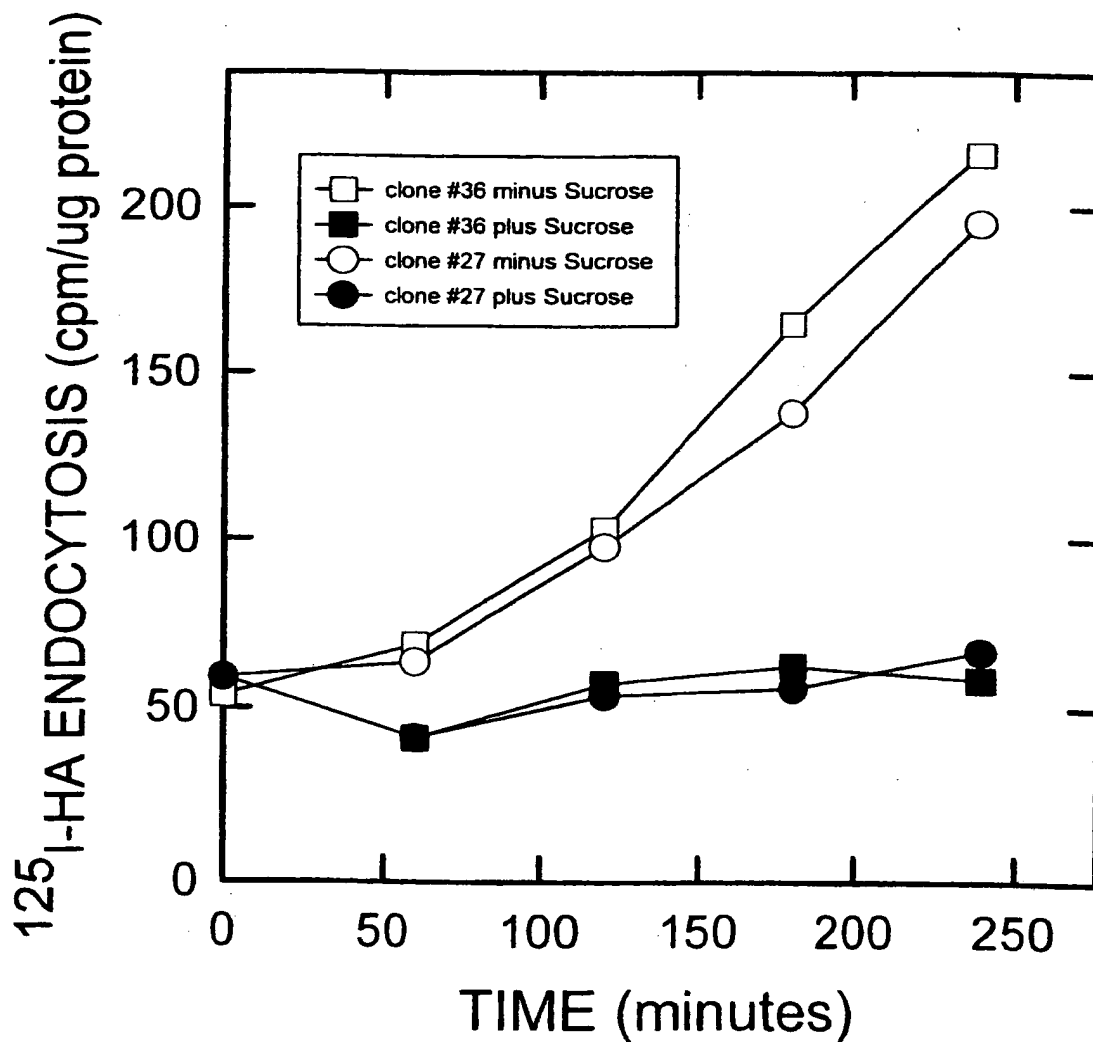


Figure 27D

**Specific monoclonal antibodies against HARE  
inhibit HA endocytosis in SK-Hep1  
transfectants expressing the 175-kDa HARE**

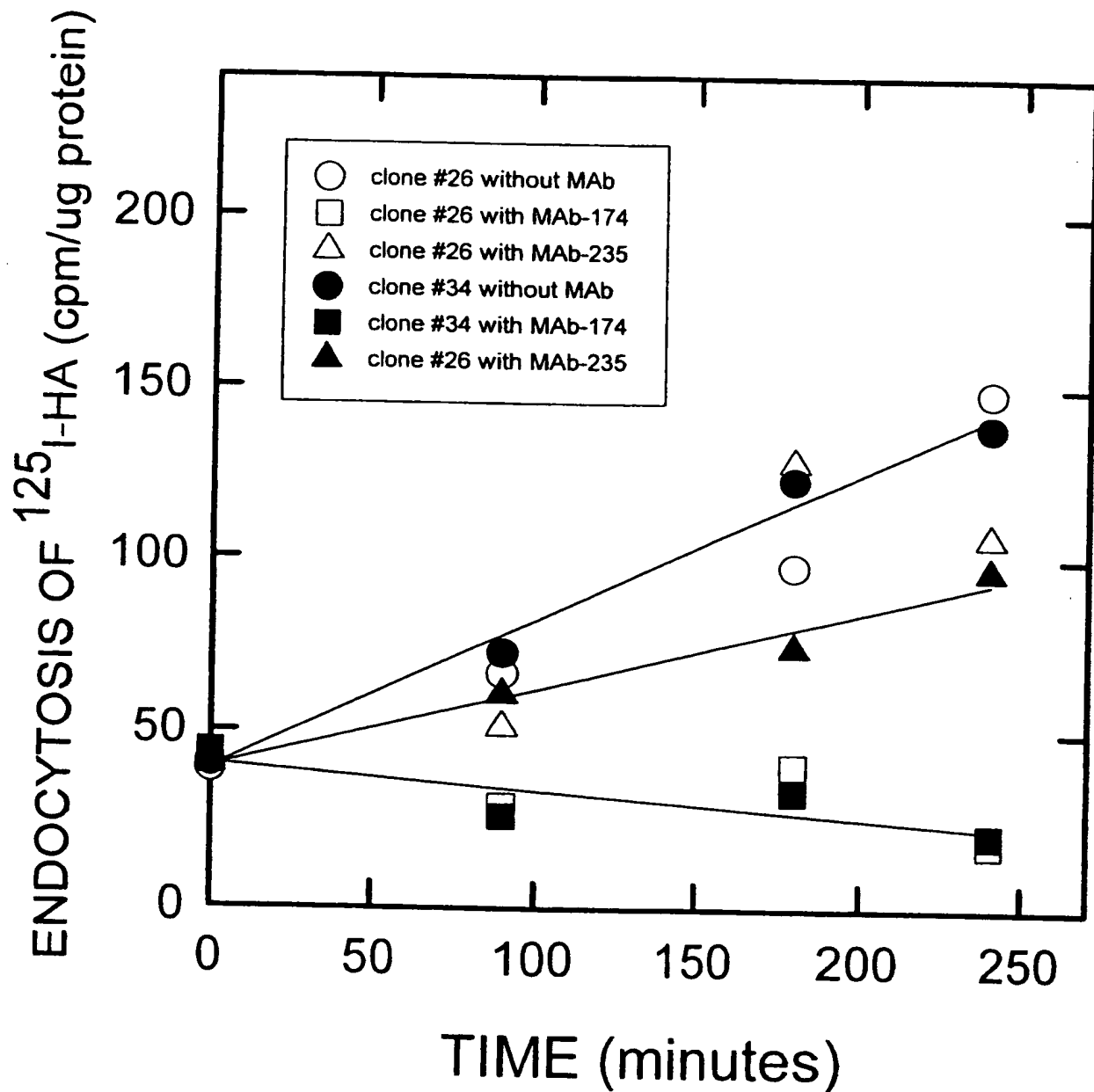


Figure 28

175SHARE	1	-----SLPS	LLTRLEQMPD	YSIFRGYI	YH	YNLASAI	ESA	DAYTVFV	PNN	EAIENV	IREK	KATSLKED	IL	RYHVVLG	EKL	LKNDLHNG	MH	RETMFGSYL											
CAB61827	1111	LHILSOVLLP	PRGDVFGGQ	LLQQLDLV	A	FSLPRELLQ	H	GLVPOI	EAA	TAYTIFV	PTN	RSLEA	---	Q	NSSHLDAD	TV	RHHVVLG	EAL	SMETLRKGGH	RNSLLGPAHH									
BAA13377	754	LHILSOVLLP	PRGDVFGGQ	LLQQLDLV	-A	FSLPRELLQ	H	GLVPOI	EAA	TAYTIFV	PTN	RSLEA	---	Q	NSSHLDAD	TV	RHHVVLG	EAL	SMETLRKGGH	RNSLLGPAHH									
175SHARE	95	LAFFPLRNDQ	YVNEAPIN	Y	TV	NVATDKG	VIH	GLEKVL	EIQK	NR	TNNDTII	V	RGH	SO	QAF	PLETKP	LR	TRK	---	Y	SIYPMGR	KRSV	F	Q	Q	VR	TIITRA	MLA	
CAB61827	1218	IVFYNNHQQP	EWNHVPLEGP	MLEAFGRSLI	GLSGVLT	VGS	SR	LHSHAEA	LREK	VN	TR	RFR	TOGFQ	L	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	
BAA13377	861	IVFYNNHQQP	EWNHVPLEGP	MLEAFGRSLI	GLSGVLT	VGS	SR	LHSHAEA	LREK	VN	TR	RFR	TOGFQ	L	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	
175SHARE	204	SLAHNAK	PAP	GEVK	-M	YALG	TASVMDG	VNG	TOT	---	W	HLPGWS	-DG	TGV	---	W	HLPGWS	-DG	TGV	---	W	HLPGWS	-DG	TGV	---	W	HLPGWS	-DG	TGV
BAB15793	9	LTNNGG	S	FFAF	N	VTRE	DQRT	---	K	Y	-TGDG	IV	R	GS	Y	IGEL	PKN	P	ST	SO	Q	Q	Q	Q	Q	Q	Q	Q	
CAB61358	1	LTNNGG	S	FFAF	N	VTRE	DQRT	---	K	Y	-TGDG	IV	R	GS	Y	IGEL	PKN	P	ST	SO	Q	Q	Q	Q	Q	Q	Q	Q	
CAB61827	1224	FFGTLCPCP	GGLOGV	S	-G	HGQCQ	DRFLG	S	GE	H	HEGF	HGTA	EV	EL	GR	Y	GN	TR	GV	---	W	HLPGWS	-DG	TGV	---	W	HLPGWS	-DG	TGV
BAA13377	967	FFGTLCPCP	GGLOGV	S	-G	HGQCQ	DRFLG	S	GE	H	HEGF	HGTA	EV	EL	GR	Y	GN	TR	GV	---	W	HLPGWS	-DG	TGV	---	W	HLPGWS	-DG	TGV
175SHARE	313	DPDGKAS	T	AAG	F	R	G	N	G	T	V	T	A	I	N	A	E	I	S	N	G	G	S	A	K	A	I	S	N
BAB15793	90	NSDGTAS	K	AAG	F	R	G	N	G	T	V	T	A	I	N	A	E	I	S	N	G	G	S	A	K	A	I	S	N
CAB61358	3	EAUGTAS	K	AAG	F	R	G	N	G	T	V	T	A	I	N	A	E	I	S	N	G	G	S	A	K	A	I	S	N
CAB61827	1433	DSAGAST	A	AAG	F	R	G	N	G	T	V	T	A	I	N	A	E	I	S	N	G	G	S	A	K	A	I	S	N
BAA13377	1076	DSAGAST	A	AAG	F	R	G	N	G	T	V	T	A	I	N	A	E	I	S	N	G	G	S	A	K	A	I	S	N
175SHARE	422	LTNNGG	S	FFAF	N	VTRE	DQRT	---	K	Y	-TGDG	IV	R	GS	Y	IGEL	PKN	P	ST	SO	Q	Q	Q	Q	Q	Q	Q	Q	
BAB15793	199	LTNNGG	S	FFAF	N	VTRE	DQRT	---	K	Y	-TGDG	IV	R	GS	Y	IGEL	PKN	P	ST	SO	Q	Q	Q	Q	Q	Q	Q	Q	
CAB61358	112	LTNNGG	S	FFAF	N	VTRE	DQRT	---	K	Y	-TGDG	IV	R	GS	Y	IGEL	PKN	P	ST	SO	Q	Q	Q	Q	Q	Q	Q	Q	
AAF82398	1	LTNNGG	S	FFAF	N	VTRE	DQRT	---	K	Y	-TGDG	IV	R	GS	Y	IGEL	PKN	P	ST	SO	Q	Q	Q	Q	Q	Q	Q	Q	
CAB61827	1543	SKNNGG	S	FFAF	N	VTRE	DQRT	---	K	Y	-TGDG	IV	R	GS	Y	IGEL	PKN	P	ST	SO	Q	Q	Q	Q	Q	Q	Q	Q	
BAA13377	1186	SKNNGG	S	FFAF	N	VTRE	DQRT	---	K	Y	-TGDG	IV	R	GS	Y	IGEL	PKN	P	ST	SO	Q	Q	Q	Q	Q	Q	Q	Q	
175SHARE	528	VG	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q		
BAB15793	305	VA	H	O	L	L	E	N	A	T	S	I	S	V	S	O	Q	T	V	I	N	N	K	A	I	S	N	G	
CAB61358	218	VA	H	O	L	L	E	N	A	T	S	I	S	V	S	O	Q	T	V	I	N	N	K	A	I	S	N	G	
AAF82398	10	VA	H	O	L	L	E	N	A	T	S	I	S	V	S	O	Q	T	V	I	N	N	K	A	I	S	N	G	
CAB61827	1648	VG	R	L	R	L	R	S	E	D	L	L	E	N	A	T	S	I	S	V	S	O	Q	T	V	I	N	N	K
BAA13377	1291	VG	R	L	R	L	R	S	E	D	L	L	E	N	A	T	S	I	S	V	S	O	Q	T	V	I	N	N	K
175SHARE	638	HTPVTW	F	W	M	P	T	D	A	L	E	A	L	P	E	Q	D	F	L	N	O	N	K	K	L	E	A	L	P
BAB15793	415	HTPVTW	F	W	M	P	T	D	A	L	E	A	L	P	E	Q	D	F	L	N	O	N	K	K	L	E	A	L	P
CAB61358	328	HTPVTW	F	W	M	P	T	D	A	L	E	A	L	P	E	Q	D	F	L	N	O	N	K	K	L	E	A	L	P
AAF82398	120	HTPVTW	F	W	M	P	T	D	A	L	E	A	L	P	E	Q	D	F	L	N	O	N	K	K	L	E	A	L	P
CAB61827	1758	HRPFTW	L	M	P	T	D	A	L	E	A	L	P	E	Q	D	F	L	N	O	N	K	K	L	E	A	L	P	
BAA13377	1401	HRPFTW	L	M	P	T	D	A	L	E	A	L	P	E	Q	D	F	L	N	O	N	K	K	L	E	A	L	P	
175SHARE	748	PTLQGR	D	T	F	T	F	D	A	S	-G	GS	V	N	T	P	S	P	R	N	S	K	P	K	G	V	Q	K	
BAB15793	525	PTLQGR	D	T	F	T	F	D	A	S	-G	GS	V	N	T	P	S	P	R	N	S	K	P	K	G	V	Q	K	
CAB61358	438	PTLQGR	D	T	F	T	F	D	A	S	-G	GS	V	N	T	P	S	P	R	N	S	K	P	K	G	V	Q	K	
AAF82398	230	PTLQGR	D	T	F	T	F	D	A	S	-G	GS	V	N	T	P	S	P	R	N	S	K	P	K	G	V	Q	K	
CAB61827	1867	PTLQGR	D	H	E	T	R	P	L	R	I	N	T	S	I	G	L	E	P	H	E	T	R	P	L	R	I	N	T
BAA13377	1510	PTLQGR	D	H	E	T	R	P	L	R	I	N	T	S	I	G	L	E	P	H	E	T	R	P	L	R	I	N	T
175SHARE	833	TPNRRGM	R	D	L	T	F	M	G	T	L	E	N	A	T	S	I	S	V	S	O	Q	T	V	I	N	N	K	
BAB15793	609	TPNRRGM	R	D	L	T	F	M	G	T	L	E	N	A	T	S	I	S	V	S	O	Q	T	V	I	N	N	K	
CAB61358	522	AP	N	N	R	G	V	L	D	O	Y	S	A	T	G	E	K	N	I	G	F	N	G	T	A	E	K	N	
AAF82398	314	AP	N	N	R	G	V	L	D	O	Y	S	A	T	G	E	K	N	I	G	F	N	G	T	A	E	K	N	
CAB61827	1977	SP	S	R	G	V	M	D	G	M	S	S	G	Q	L	L	R	S	C	F	A	G	T	A	E	K	N		
BAA13377	1620	SP	S	R	G	V	M	D	G	M	S	S	G	Q	L	L	R	S	C	F	A	G	T	A	E	K	N		
175SHARE	943	IT	T	V	D	R	K	Q	I	N	G	G	A	K	V	A	R	S	O	K	G	T	R	V	S	K	G	T	
BAB15793	719	IT	T	V	D	R	K	Q	I	N	G	G	A	K	V	A	R	S	O	K	G	T	R	V	S	K	G	T	
CAB61358	632	IT	T	V	D	R	K	Q	I	N	G	G	A	K	V	A	R	S	O	K	G	T	R	V	S	K	G	T	
AAF82398	424	IT	T	V	D	R	K	Q	I	N	G	G	A	K	V	A	R	S	O	K	G	T	R	V	S	K	G	T	
CAB61827	2087	RV	T	V	A	D	L	O	D	G	H	G	S	E	H	A	N	S	O	V	G	T	M	V	T	S	K	G	
BAA13377	1730	RV	T	V	A	D	L	O	D	G	H	G	S	E	H	A	N	S	O	V	G	T	M	V	T	S	K	G	
175SHARE	1052	JADLYFQD	T	VG	F	L	R	S	P	L	G	O	Y	K	L	T	F	D	K	A	R	E	A	N	E	A	A	T	
BAB15793	828	JADLYFQD	T	VG	F	L	R	S	P	L	G	O	Y	K	L	T	F	D	K	A	R	E	A	N	E	A	A	T	
CAB61358	741	JADLYFQD	T	VG	F	L	R	S	P	L	G	O	Y	K	L	T	F	D	K	A	R	E	A	N	E	A	A	T	
AAF82398	533	JADLYFQD	T	VG	F	L	R	S	P	L	G	O	Y	K	L	T	F	D	K	A	R	E	A	N	E	A	A	T	
CAB61827	2197	TQDHPQEK	R	AG	V	F	H	L	R	S	P	L	G	O	Y	K	L	T	F	D	K	A	R	E	A	N	E	A	A
BAA13377	1840	TQDHPQEK	R	AG	V	F	H	L	R	S	P	L	G	O	Y	K	L	T	F	D	K	A	R	E	A	N	E	A	A
175SHARE	1162	IKAGYVGD	G	F	S	-	SGNLL	QVLSF	F	P	S	L	T	N	F	L	T	E	V	L	A	S	K	S	A	R	G	A	F
BAB15793	938	IKAGYVGD	G	F	S	-	SGNLL	QVLSF	F	P	S	L	T	N	F	L	T	E	V	L	A	S	K	S	A	R	G	A	F
CAB61358	849	IKAGYVGD	G	F	S	-	SGNLL	QVLSF	F	P	S	L	T	N	F	L	T	E	V	L	A	S	K	S	A	R	G	A	F
AAF82398	643	IKAGYVGD	G	F	S	-	SGNLL	QVLSF	F	P	S	L	T	N	F	L	T	E	V	L	A	S	K	S	A	R	G	A	F
CAB61827	2307	IKAGYVGD	G	F	S	-	SGNLL	QVLSF	F	P	S	L	T	N	F	L	T	E	V	L	A	S	K	S	A	R	G	A	F
BAA13377	1950	IKAGYVGD	G	F	S	-	SGNLL	QVLSF	F	P	S	L	T	N	F	L	T	E	V	L	A	S	K	S	A	R	G	A	F
175SHARE	1271	LITAS	-	-	Q	D	Q	L	H	-	E	T	R	F	V	D	R	S	I	L	O	W	D	I	A	I	A	N	G
BAB15793	1047	LITAS	-	-	Q	D	Q	L	H	-	E	T	R	F	V	D	R	S	I	L	O	W	D	I	A	I	A	N	G
CAB61358	924	LITAS	-	-	Q	D	Q	L	H	-	E	T	R	F	V	D	R	S	I	L	O	W	D	I	A	I	A	N	G
AAF82398	752	LITAS	-	-	Q	D	Q	L	H	-	E	T	R	F	V	D	R	S	I	L	O	W	D	I	A	I	A	N	G
CAB61827	2416	IISDAGPDS	SWAPV	AG	T	V	W	S	R	I	I	W	D	I	A	I	A	N	G	-	-	-	-	-	-	-	-	-	
BAA13377	2059	IISDAGPDS	SWAPV	AG	T	V	W	S	R	I	I	W	D	I	A	I	A	N	G	-	-	-	-	-	-	-	-	-	
175SHARE	1370	LASSP	-	RIS	Q	T	L	C	M	R	P	O	R	R	H	P	O	S	P	E	V	T	P	S	Q	T	L		

Figure 29

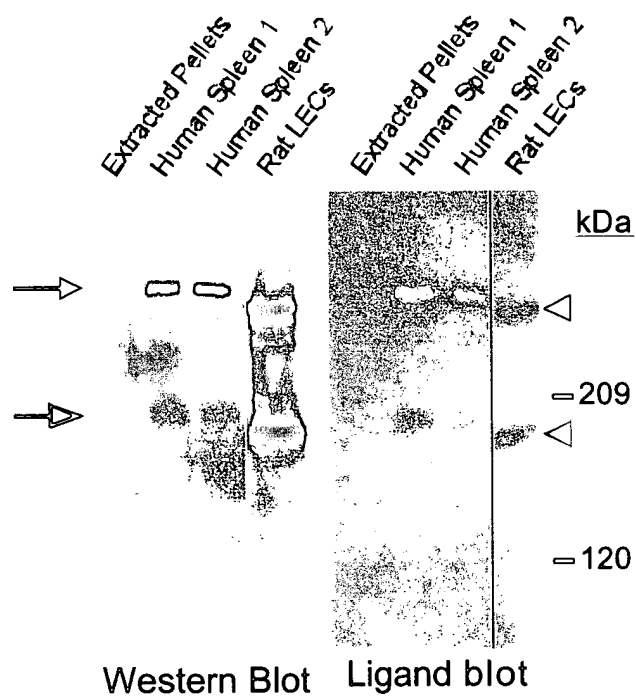
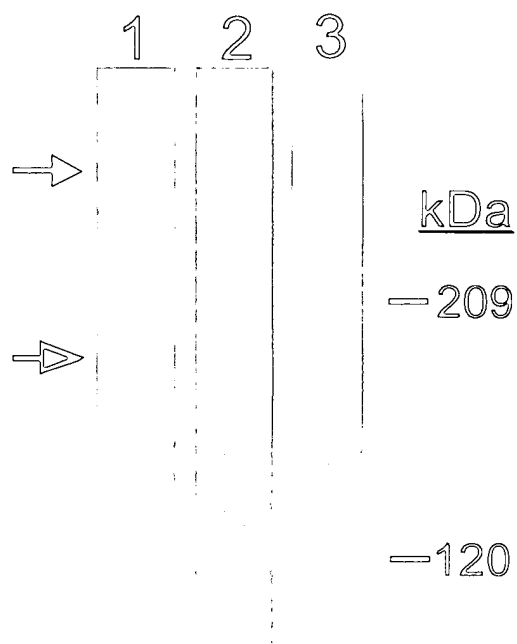
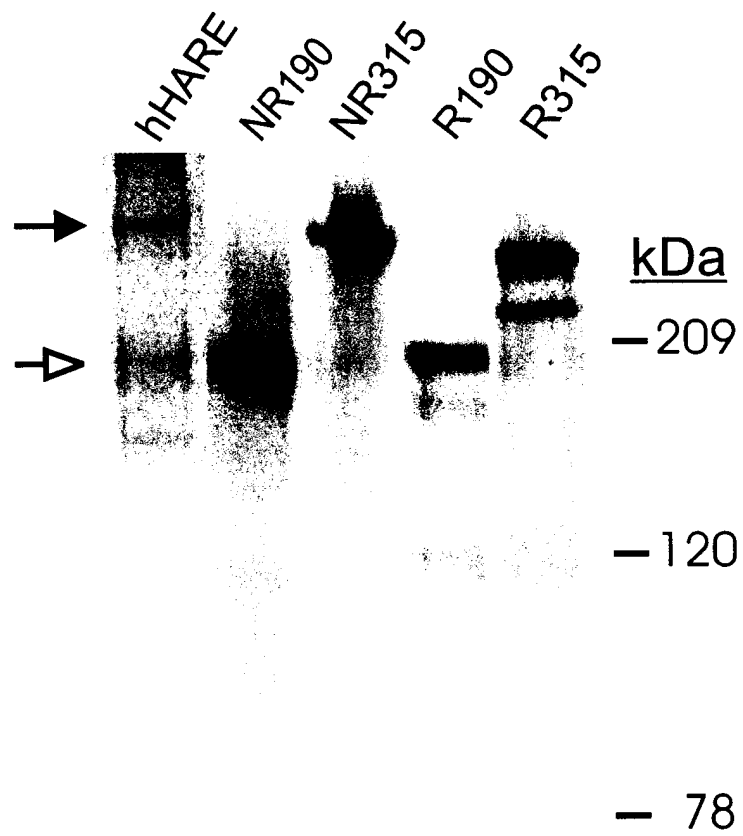




Figure 3 0



# Figure 31



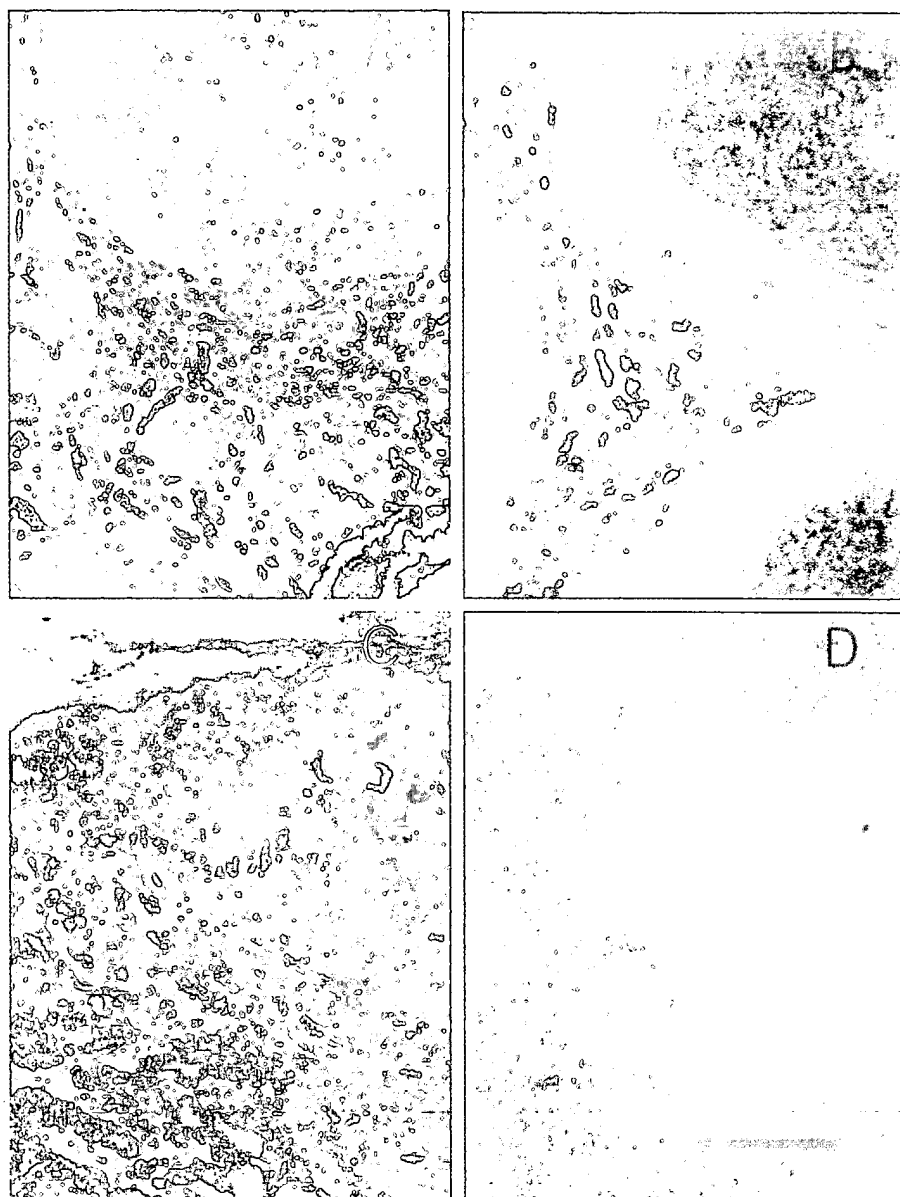






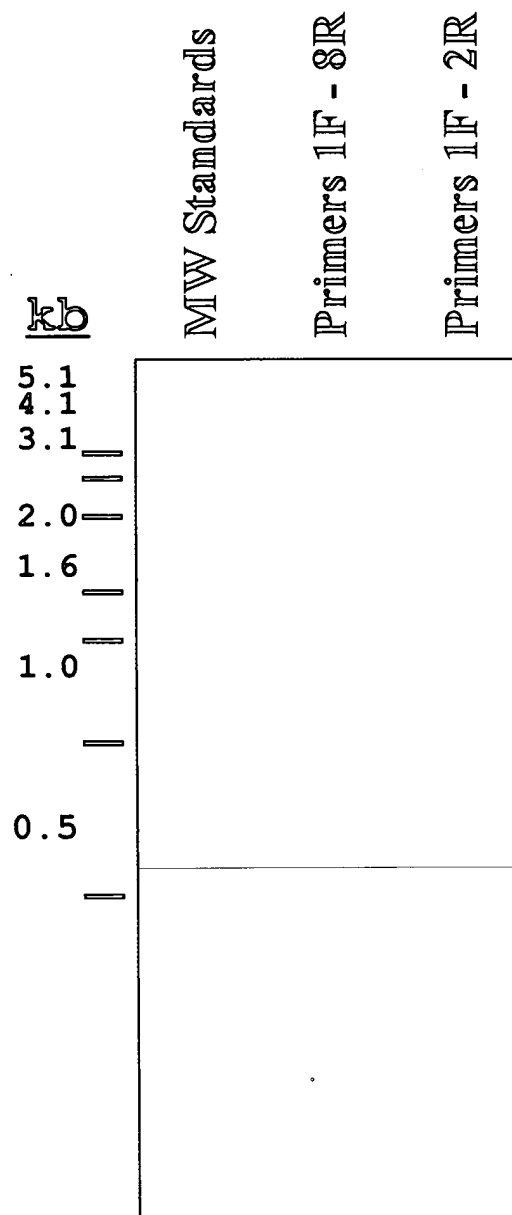
Figure 35

1 IOYNLANAIEAADAYTVFAP NNAIENYIREKKVLSLEED VLRYHVVLEEKLLKNDLHNG MHRETMLGFSYFLSFFLHND QLYVNEAPINTNNVATDKGV  
 23 IHNLASAIESADAYTVFVP NNEAIENYIREKATSLKED ILRYHVVLGEKLLKNDLHNG MHRETMLGFSYLLAFLRND QLYVNEAPINTNNVATDKGV  
 101 IHGLGKVLLEIOKNNNDNDN TTIIRGRERTSSSELTTPFGT KSLGNEKRRRIYTSYFMGRR TLFIGQPKQVVRTVITREPC AGFFGPOCQPCPGNAQNVCF  
 123 IHGLEKVLLEIOKNNNDNDN IIVRGECKSQAPPLET KPL-RETRKRIYSIYFMGR SVFIGQPKQVVRTIITRAGW LASLAHNAKPAPEVGMKAL  
 201 GNGICLDGVNGTGTBEGEG FSGTAEETTEGKYGIHDDQ ASQVHGRNQOPLGDGSDP DDVGMRGVHNDNATTEDNCA QCHTSANGLTNSDGTASPK  
 222 GTASVMDGVNGTGTBEGGLG FNGTAEETTEGKYGIHDDQ ASQVHGRNQOPLGDGSDP DDVGMRGVHNDMEITTDNCA QCHTSANGLLDPPDGKASPK  
 301 AAGFOCNGTGTAINADEI SNGGSAKADKRTTPGRRV TTKAGYTGDIIVLEINP LKAGYTDKNAEQTOTGPNQ AANLPLPAYTGDGKVPTLIN  
 322 AAGFRNGTGTAINADET SNGGSTKADKRTTPGNRV BVKAGYTGDIIVLEINP BVKAGYTDKNAEQTOTGPNQ AVNGLPKYTGDKVPSLIN  
 401 VLTKNNGGSEFAICNNT Q VERTTKKPNYIGDGTARG SIYQELPKNPKTSQYFFQLQ EHFVKDLVGPGFVTFAPLS AAFDEARVKDWDKYGLMPQ  
 422 VLTNNNGGSPFAFCNNT Q DQRIKPKDYTGDIIVRG SIYGELPKNPKTSQYFFQLQ EHAVRELAGPGFTVTFAPLS SSFNHEPRIKDWDOQGLMSQ  
 501 VLRYHVVAHQLLLENLKI SNATSLQGEPIVISVSQSTV YINNKAIISSDIISTNGIV HIIDKLLSPKNLLITPKDNS GRILQNTTTLATNNGYIKFS  
 522 VLRYHVVGQQLLLDLNLKVT TSATTLQGEPIVISVSQSTV FINNEAKVLSDDIISTNGVI HVIDKLLSPKNLLITPKDAL GRVLQNTTVAANHGYTKFS  
 601 NLIQDSGLLSVITDPIHTPV TLFWPTDQALHALPAEQQDF LFNQDNKDKLEYLKEHVIR DAKVLAVDLPSTAWKTLOG SELSVKQAGARDIGDLFLNG  
 622 KLIQDSGLLSVITDSIHTPV TVFWPTDKALEALPPEQQDF LFNQDNKDKLSYLKEHVIR DSKALASDLPRASAMKTLOG SELSVRQGTGSDIGELFLNE  
 701 QTRIVQRELLFDLGVAAYGI DALLIDPTLGGRTDTFTFD ASGESGVNTVPSPRWSKP KGVKQQLYN-LPFRKNLEG RERPSLVIQIPRCQKGYFG  
 722 QMRFTHRGLLFDVGVAAYGI DALLMNPTLGGRTDTFTFD IPGECSGIIFTPKPLKSKP KGVKKKKIYNPLPFRNVEG QNLIVVIQTPRCGHGYFM  
 800 RDQAPGPGPDAPPNNRGV LDQYSATGEKNTGFCNNTA DEMWPGRFGPDLPCGSD HGQDDGITSGGQPLGETGW TGPSDDTQAVLPVAVTTPPS  
 822 PDQAPGPGPDPNNRGV RDLYTPMGQDHTGFCNNTA BELWHRGFRGPDQPRSE HGQDEGITSGGQPLGETGW TAASDDTPTAVFANGTPAS  
 900 AHATCKENNGEENLDYEGD GITTVVDFPKQDNGGQAKV ARQSKGTQVSSQKGYK DGHSTEIDPADGLNGGCH EHATQKMTGPGKHKEKSH  
 922 VHATCKENNGEENLDYEGD GITTVVDFPKQDNGGQAKV AKQSKGTQVSSQKGYK DGYSEIDPADGVNGGCH EHATQKMTGPGKHKEKSH  
 1000 YVGDGLNPEPOLPIDRLQ DNGQHADAKQVDLHFQDIT VGVFHLRSPLGQYKLTFDKA REANEAAATMATYNQLSYA QKAKYHLASAGWLETGRVAY  
 1022 YVGDGVDPEPOLPLDRQLQ DNGQHHPDASADLYFQDIT VGVFHLRSPLGQYKLTFDKA KEAPAKEAATMATYNQLSYA QKAKYHLASAGWLESGRVAY  
 1100 PTAFASQNGSVVGIVDYG PRPKBEMDVFVYRMKDVN PTKKGYVYVGDGFSQGNLLQ VLMSFPLTNFLTEVLAYSN SSARGRAFLEHLDLDSIRGT  
 1122 PTYASQKGANVVGIVDYG SRANKBEMDVFVYRMKDVN PTKKAGYVYVGDGFSQGNLLQ VLMSFPLTNFLTEVLAFSK SSARGQAFLEHLDLDSIRGT  
 1200 LFVPQNSGLGENETLSGRDI EHLHANVSMFFYNDLVNNT EHLRLGSKLLITASODPLOP TETRFVDGRAILOWDIFASN GIHVISRPLKAPPAPVTLT  
 1222 LFVPQNSGLPGNKSLSGRDI EHLTNVNVSYNDLVNNT LRTMLGSQLLITFSODQLHQ -ETRFVDGRSILQWDIIAAN GILHIISEPLRAPPTAATA  
 1300 HTGLGAGITFAILLVTGAIA LAANSYFRINRRTIGFOHFE SEEDINVAALGKQOOPENISN PLTESTSAPPEPSDDPFTD SEEROLEGNDPLRTL  
 1321 HSLGLTGIFCAVVLVTGAIA LAANSYFRILKQRTGFORFD QKRTILMSWLLASSPRISQ LCMRPQRRHPQSPVPSPSQT LENRIWRTAGLWGHGCPDMR  
 1421 SQATTVTTVPR



# Figure 37

Amplification of the 1394 amino acid HARE  
Open Reading Frame from a human lymph  
node cDNA Library





# Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12  
(encoding 1357 of the 1394 amino acids disclosed here)

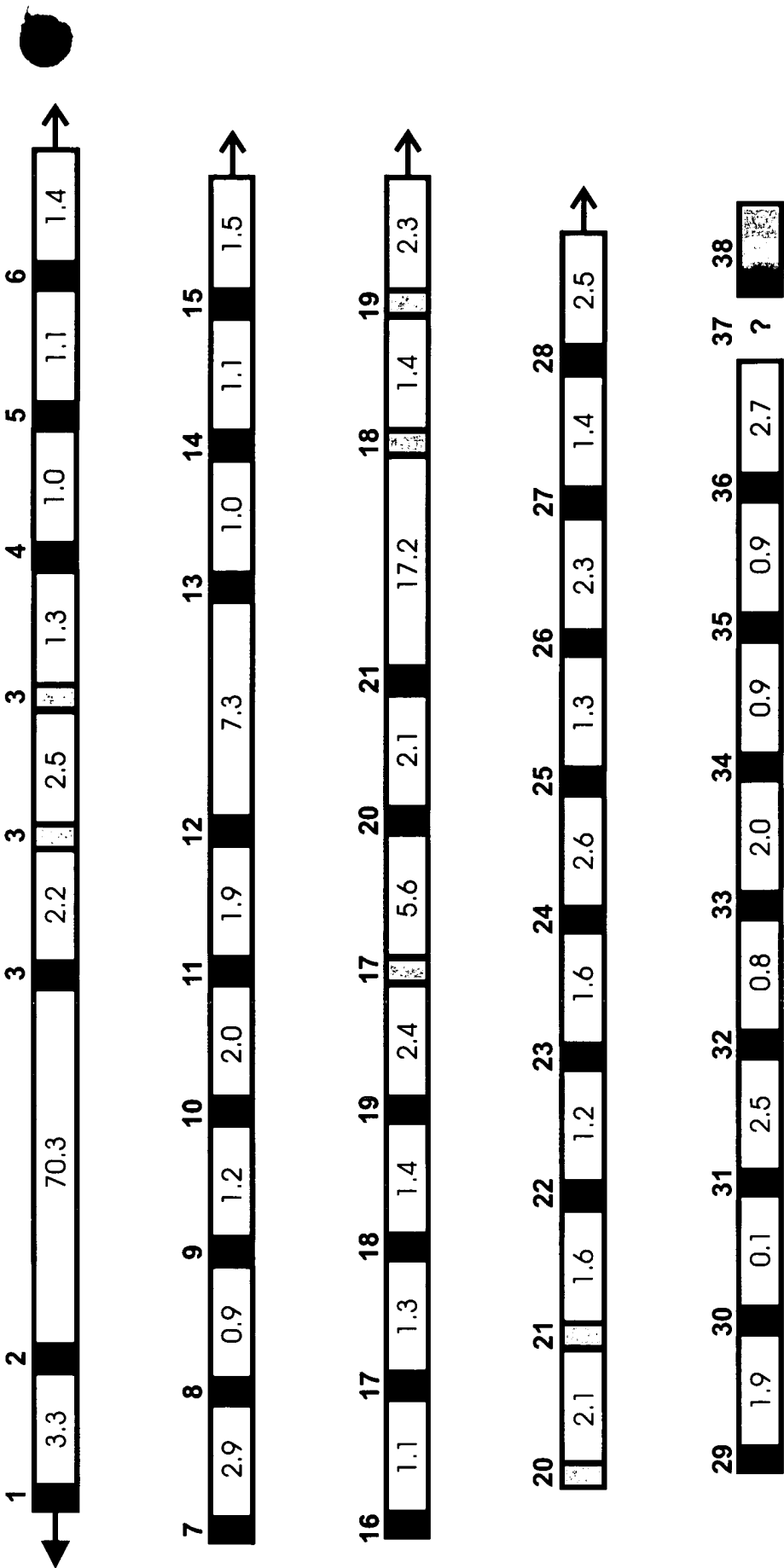


Figure 3 9

